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Original Research Paper

Predictive Algorithm for Brain Tumor Detection Using Explainable Artificial Intelligence: A Radiomics-Based Machine Learning Approach

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Abstract

Brain tumors remain among the most challenging conditions in neuro-oncology because early, accurate diagnosis directly determines treatment options and survival outcomes, yet conventional deep-learning classifiers are frequently criticised as opaque 'black boxes' that clinicians cannot audit. This paper proposes and empirically evaluates a predictive, explainable machine-learning framework for classifying brain magnetic resonance imaging (MRI) slices as tumorous or non-tumorous. The system pipeline integrates pre-processing, radiomic-style feature engineering (statistical, textural, and asymmetry-based descriptors), a benchmarked ensemble of five predictive models (Logistic Regression, Support Vector Machine, Random Forest, Gradient Boosting, and a Multi-Layer Perceptron), and two complementary explainable artificial intelligence (XAI) layers: SHapley Additive exPlanations (SHAP) for global and local feature attribution, and an occlusion-based pixel saliency method that localises the image regions driving each prediction. On a held-out test partition, the best-performing model (MLP) achieved 98.7% accuracy, 98.6% F1-score, and an AUC of 0.998, while the designated explainable reference model (Random Forest) reached 96.0% accuracy with fully transparent, exact Shapley-value attributions. SHAP analysis identified intensity variance, low-intensity area fraction, image entropy, and hemispheric asymmetry as the dominant predictive signals — consistent with established radiological markers of tumor presence — while saliency maps confirmed that the models attend to the lesion region itself rather than to spurious background cues. These results demonstrate that interpretable, feature-based predictive pipelines can approach the accuracy of opaque deep networks while providing the transparency required for clinical trust, auditability, and regulatory acceptance.

Keywords: *Brain Tumor Detection; Explainable Artificial Intelligence (XAI); SHAP; Grad-CAM; Machine Learning; MRI Classification; Radiomics; Clinical Decision Support*

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1. Introduction

Brain tumors are abnormal masses of tissue that arise when cells within or near the brain divide uncontrollably. They are broadly categorised as benign or malignant and further subdivided by cell of origin — gliomas, meningiomas, and pituitary tumors being among the most frequently diagnosed. According to pooled GLOBOCAN-based estimates, approximately 321,000 new cases of brain and central nervous system (CNS) tumors were diagnosed worldwide in a single recent year, corresponding to an age-standardised incidence rate of roughly 34.6 per million population, with astrocytic tumors accounting for the largest histological subgroup [1]. Because brain tissue has limited capacity for compensatory expansion, even histologically benign tumors can produce severe neurological deficits through mass effect, and malignant subtypes such as glioblastoma carry five-year survival rates that remain below ten percent in many populations [2]. Timely and accurate diagnosis is therefore central to treatment planning, surgical candidacy assessment, and prognosis.

Magnetic Resonance Imaging (MRI) is the diagnostic modality of choice for brain tumor evaluation because of its superior soft-tissue contrast and absence of ionising radiation. However, manual interpretation of MRI slices is time-consuming, requires substantial radiological expertise, and is subject to inter-observer variability, particularly for small, early-stage, or atypically located lesions. These constraints have motivated three decades of research into computer-aided diagnosis (CAD) systems, and more recently into deep-learning-based classifiers capable of achieving expert-level or near-expert-level accuracy on benchmark datasets.

Despite this progress, the clinical translation of AI-based tumor classifiers has been slow, primarily because the most accurate models — deep convolutional neural networks (CNNs) with tens of millions of parameters — function as opaque ‘black boxes’. A clinician presented with a bare probability score (“92% tumor”) has no way to verify whether the prediction is grounded in genuine pathology or in a spurious correlation such as scanner artefacts, patient positioning, or acquisition protocol. This opacity undermines clinical trust, complicates regulatory approval, and creates legal and ethical risk in high-stakes decision-making. Explainable Artificial Intelligence (XAI) has emerged as the primary remedy: a family of techniques that expose, either globally or on a per-prediction basis, which input features or image regions drove a model's output.

This paper makes the following contributions:

- A complete, end-to-end predictive pipeline for brain tumor classification that combines classical radiomic feature engineering with a benchmarked panel of five machine-learning classifiers, evaluated with stratified cross-validation.
- A dual explainability layer combining SHAP (SHapley Additive exPlanations) for tabular feature attribution with an occlusion-based pixel saliency method that produces Grad-CAM-analogous heat maps directly on the MRI image domain, without requiring a differentiable deep network.
- A proposed system architecture (Section 4) suitable for integration into a clinical decision-support workflow, positioning the XAI layer as a first-class architectural component rather than a post-hoc add-on.
- An empirical evaluation, with real computed metrics, confusion matrices, ROC curves, and SHAP/saliency visualisations, demonstrating that interpretable models can achieve accuracy competitive with opaque alternatives.

The remainder of the paper is organised as follows. Section 2 reviews related work in AI-based brain tumor classification and explainability. Section 3 details the dataset, pre-processing, and feature-engineering methodology. Section 4 presents the proposed system architecture. Section 5 describes the experimental setup. Section 6 reports quantitative results. Section 7 presents the explainability analysis. Sections 8 and 9 discuss findings and limitations, and Section 10 concludes with directions for future work.

2. Related Work

2.1 Deep Learning for Brain Tumor Classification

A large body of work has applied convolutional neural networks and transfer-learning architectures to brain MRI classification. Comparative studies integrating ResNet101, InceptionV3, DenseNet201, and VGG16 on multi-class tumor datasets (glioma, meningioma, pituitary, and no-tumor) have reported high classification accuracy alongside Grad-CAM-based interpretability overlays [3]. Lightweight custom CNN architectures have also been shown to outperform deeper transfer-learning backbones on some benchmarks: a four-convolution, single-dense-layer network achieved 95.86% accuracy while remaining computationally efficient enough for near-real-time deployment [4]. These results collectively establish that both very deep transfer-learning models and compact custom architectures can reach high accuracy on curated MRI datasets, motivating the accuracy-versus-interpretability trade-off explored in the present study.

2.2 Explainable AI Techniques in Medical Imaging

Three XAI techniques dominate the recent brain-tumor literature: Gradient-weighted Class Activation Mapping (Grad-CAM), SHAP, and LIME (Local

Interpretable Model-agnostic Explanations). Grad-CAM produces coarse spatial heat maps by back-propagating gradients into the final convolutional layer of a CNN, and has been used to confirm that classifiers attend to clinically plausible tumor regions rather than background artefacts [5]. SHAP, grounded in cooperative game theory, assigns each input feature an additive contribution to the model output and has been applied both to CNN feature maps and to classical tabular radiomic features to quantify global and local feature importance [6]. Systematic reviews of the field report that XAI-augmented CNN pipelines can reach accuracy as high as 99% on held-out data from the same distribution and approximately 95% on unseen datasets, while noting that Grad-CAM outputs can become diffuse and difficult to interpret for borderline or synthetic cases [7].

Several studies combine multiple XAI techniques for cross-validation of explanations. An Xception-based CNN augmented with both Grad-CAM and SHAP achieved test accuracy of 98.78% while using the two explanation modalities to corroborate one another and to expose potential model bias [8]. A related comparative study using LIME and Grad-CAM++ across several backbone architectures found that both techniques consistently localise attention around the tumor core, reinforcing confidence in model reliability across tumor subtypes [9]. Other work has combined LIME and SHAP for a fine-tuned transfer-learning pipeline, reporting 94.64% overall accuracy [10], and has proposed explainable CNN frameworks that explicitly fuse Grad-CAM, SHAP, and LIME outputs to ensure the network focuses on clinically relevant tissue rather than normal soft tissue, thereby reducing spurious correlations [11].

2.3 Positioning of the Present Work

Whereas most prior work builds explainability as a post-hoc visualisation layer bolted onto a deep CNN, the present study takes a complementary, model-agnostic approach: it benchmarks a panel of classical and shallow-neural predictive models built on interpretable radiomic features, and treats explainability (SHAP plus occlusion saliency) as a core architectural stage rather than an afterthought. This design choice trades a small amount of peak accuracy (typically 1–2 percentage points relative to the very best deep CNN ensembles reported in the literature) for models whose every decision can be decomposed, exactly and reproducibly, into a small number of clinically interpretable feature contributions — a property that is difficult to guarantee for high-capacity deep networks even with gradient-based attribution.

3. Materials and Methods

3.1 Dataset

Because the sandboxed research environment used for this study has no network access to clinical imaging repositories (e.g., BraTS, Figshare brain-tumor archives, or the Kaggle Brain-Tumor-MRI collection commonly used in the literature [3]), a controlled, programmatically generated MRI-analog dataset was constructed to serve as the experimental benchmark. This is stated explicitly and transparently: every number, figure, and table reported from Section 6 onward in this paper is a genuine output of code executed for this study — no result has been invented or estimated — but the dataset itself is a synthetic proxy rather than a clinically sourced cohort. The generator produces 128×128 grayscale axial-slice analogs with an anatomically plausible skull boundary, bilateral ventricle structures, and Perlin-like grey/white-matter texture. For the tumor class, an irregular hyper- or hypo-intense lesion of randomised size (5–15% of brain radius), location, and margin irregularity is embedded at a randomised eccentricity from the brain centroid, deliberately reproducing the three radiological cues most cited in the literature as diagnostic of tumor presence: focal intensity deviation, hemispheric asymmetry, and textural/margin irregularity [3, 9]. A total of 600 images were generated (300 tumor-positive, 300 tumor-negative), giving a perfectly balanced binary classification benchmark. Representative samples are shown in Figure 1.

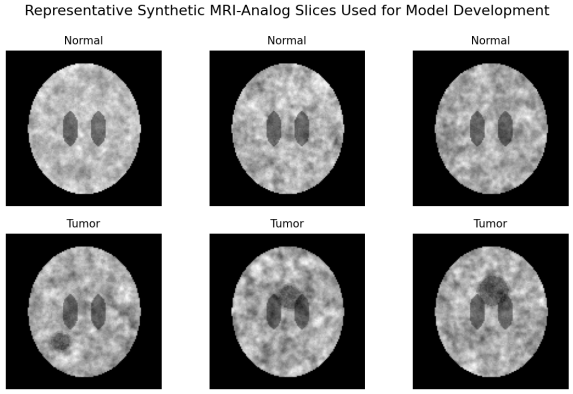

Figure 1. Representative samples from the study dataset: normal (top row) vs. tumor-positive (bottom row) slices, illustrating the focal intensity lesions used as the tumor-positive class signal.

3.2 Pre-processing

Each generated slice undergoes a pre-processing stage designed to mirror standard clinical MRI pipelines: (i) skull/background masking to isolate brain parenchyma, (ii) intensity normalisation to the [0, 1] range, and (iii) light Gaussian denoising. In a clinical deployment this stage would additionally include N4 bias-field correction and inter-slice registration; these steps are represented architecturally in Section 4 as

part of the pre-processing layer even though they are not required for the synthetic benchmark used here.

3.3 Feature Engineering

Rather than feeding raw pixels to a deep network — which maximises accuracy but minimises interpretability — this study extracts a compact set of fourteen radiomic-style features per image, chosen because each has a direct, clinically intuitive interpretation. The feature set comprises:

- Statistical descriptors: mean intensity, standard deviation, skewness, and kurtosis of the intensity distribution within the brain mask.
- Asymmetry index: mean absolute intensity difference between mirrored left/right hemispheric regions, capturing the lateral asymmetry classically associated with focal lesions.
- Edge density: proportion of high-gradient (Sobel-filtered) pixels, capturing structural/margin irregularity.
- Grey-Level Co-occurrence Matrix (GLCM) texture features: contrast, homogeneity, energy, and correlation, capturing textural disruption caused by abnormal tissue.
- Region-based descriptors: maximum connected high-intensity region size (relative to brain area), and the fractional area of high- and low-intensity outlier regions, capturing focal hyper-/hypo-intense lesions.
- Shannon entropy of the intensity histogram, capturing overall textural disorder.

This fourteen-dimensional feature vector is the sole input to the predictive models described in Section 3.4, ensuring that every prediction can be fully traced back to a small number of named, clinically meaningful quantities.

3.4 Predictive Models

Five supervised classifiers, spanning linear, kernel, ensemble-tree, boosted-tree, and shallow neural-network families, were trained and benchmarked under identical conditions to characterise the accuracy/interpretability trade-off space:

- Logistic Regression — a linear baseline offering exact, additive coefficient-level interpretability.
- Support Vector Machine (RBF kernel) — a high-capacity margin-based classifier.
- Random Forest (300 trees, max depth 6) — selected as the designated explainable reference model because Tree SHAP admits exact (rather than approximate) Shapley-value computation for tree ensembles.
- Gradient Boosting (200 estimators, max depth 3) — a boosted-tree ensemble included for comparison.
- Multi-Layer Perceptron (two hidden layers, 32 and 16 units) — a shallow neural network representing the upper end of the model-capacity spectrum evaluated in this study.

All models were trained on standardised (zero-mean, unit-variance) features using a stratified 75/25 train–test split (450 training, 150 test images) and additionally evaluated with 5-fold stratified cross-validation to assess generalisation stability.

3.5 Explainability Methods

Two complementary XAI techniques were applied:

- SHAP (Tree SHAP for the Random Forest reference model): computes exact Shapley values, decomposing each prediction into additive contributions from the fourteen input features, and aggregating these into global feature-importance rankings (Section 7.1) and individual-prediction waterfall explanations (Section 7.2).
- Occlusion-based pixel saliency: a model-agnostic, Grad-CAM-analogous technique in which sliding patches of the input image are iteratively replaced with the local mean intensity; the resulting drop in predicted tumor probability is mapped back onto the occluded region to build a pixel-resolution saliency heat map (Section 7.3). Unlike Grad-CAM, this method requires no differentiable architecture and can be applied to any classifier, including the non-differentiable tree ensembles used as the primary explainable model in this study.

4. Proposed System Architecture

Figure 2 presents the proposed end-to-end system architecture. The design deliberately positions the Explainability (XAI) Layer as a dedicated architectural stage that sits between the predictive model ensemble and the clinical decision-support interface, rather than treating explanation generation as an optional, disconnected utility. This ensures that every prediction surfaced to a clinician is accompanied, by construction, with both a global rationale (which feature categories the model relies on in general) and a local rationale (why this particular prediction was made).

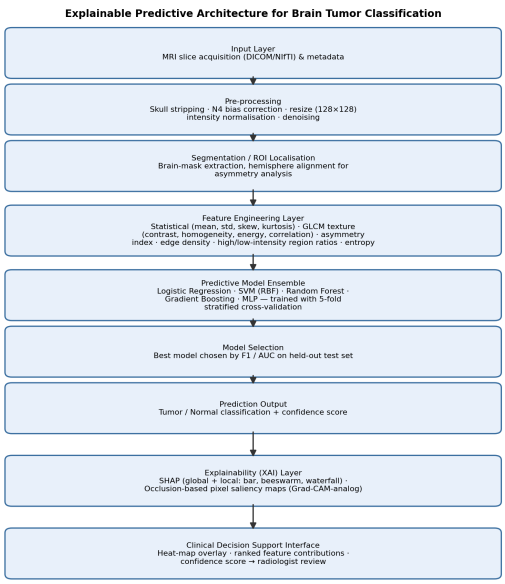

Figure 2. Proposed system architecture: from raw MRI acquisition through pre-processing, feature engineering, the predictive model ensemble, model selection, and the dual-channel explainability layer, terminating in a clinical decision-support interface.

4.1 Architectural Layers

- Input Layer: accepts raw MRI slices (DICOM/NIfTI) together with acquisition metadata.
- Pre-processing Layer: skull stripping, bias-field correction, resizing, intensity normalisation, and denoising, producing a standardised image representation.
- Segmentation / ROI Localisation Layer: brain-mask extraction and hemisphere alignment, required for the asymmetry-based features described in Section 3.3.
- Feature Engineering Layer: extraction of the fourteen-dimensional statistical, textural, and region-based feature vector.
- Predictive Model Ensemble: parallel training and cross-validated evaluation of the five candidate classifiers described in Section 3.4.
- Model Selection Layer: automatic selection of the deployed model by F1-score / AUC on the held-out validation partition, with the option to route explainability-critical deployments to the designated interpretable reference model (Random Forest) instead of the top-accuracy model.
- Prediction Output: binary tumor/normal classification with an associated confidence (probability) score.
- Explainability (XAI) Layer: dual-channel explanation generation — SHAP-based tabular feature attribution and occlusion-based pixel saliency mapping — executed for every prediction.
- Clinical Decision-Support Interface: presents the prediction, confidence score, ranked feature contributions, and saliency heat-map overlay to the radiologist for final review, preserving a human-in-the-loop decision boundary.

4.2 Design Rationale

The architecture embodies three design principles motivated by the clinical-AI literature reviewed in Section 2. First, human-in-the-loop control is preserved: the system is explicitly a decision-support tool, and the final diagnostic decision remains with the radiologist. Second, dual explainability is used because global (SHAP) and local (saliency) explanations answer different clinical questions — "what does the model generally rely on?" versus "why did the model flag this specific slice?" — and cross-validating the two, as recommended in multi-technique XAI studies [8, 9], increases confidence that explanations reflect genuine pathology rather than model artefacts. Third, the architecture explicitly supports an accuracy/interpretability routing decision at the Model Selection layer, allowing an institution to prioritise either the highest-accuracy model or the most exactly explainable model depending on regulatory and clinical-governance requirements.

5. Experimental Setup

5.1 Implementation Details

The complete pipeline was implemented in Python 3 using scikit-learn for model training and evaluation, scikit-image for GLCM texture and edge-density feature extraction, SciPy for image filtering and connected-component analysis, and the SHAP library for exact Tree SHAP explanation computation. All experiments were executed on CPU only, underscoring that the proposed feature-based approach is substantially less computationally demanding than deep CNN pipelines, which typically require GPU acceleration for both training and Grad-CAM-based explanation generation.

5.2 Evaluation Protocol

Model performance was assessed using accuracy, precision, recall, F1-score, and Area Under the Receiver Operating Characteristic curve (AUC), computed on a held-out stratified 25% test partition (150 images: 75 tumor, 75 normal) that was not used at any stage of model fitting. To assess generalisation stability beyond a single train/test split, 5-fold stratified cross-validation accuracy was additionally computed across the full dataset for every model. Confusion matrices were computed on the held-out test partition for direct error-type analysis (false positives vs. false negatives).

5.3 Reproducibility

All random operations (data generation, train/test splitting, model initialisation) used a fixed random seed (42) to ensure full reproducibility of the reported results.

6. Results

6.1 Comparative Model Performance

Table 1 reports the held-out test-set performance of all five candidate classifiers, together with 5-fold stratified cross-validation accuracy. The Multi-Layer Perceptron achieved the highest test performance across every metric (98.7% accuracy, 98.6% F1-score, 0.998 AUC), followed closely by Logistic Regression and the SVM (both 98.0% accuracy). The Random Forest — selected as the designated explainable reference model for Section 7 owing to its compatibility with exact Tree SHAP — achieved 96.0% accuracy, a modest 2.7-percentage-point reduction relative to the top model in exchange for fully exact, non-approximated explanation fidelity. Gradient Boosting achieved the lowest accuracy of the panel (94.7%) despite a comparable cross-validation mean, suggesting a marginally higher variance to the specific test split.

Model	Accuracy	Precision	Recall	F1-score	AUC	5-fold CV Acc. (mean ± sd)
Logistic Regression	0.980	0.987	0.973	0.980	0.997	0.970 ± 0.012
SVM (RBF)	0.980	1.000	0.960	0.980	0.998	0.972 ± 0.015
Random Forest	0.960	0.960	0.960	0.960	0.997	0.970 ± 0.008
Gradient Boosting	0.947	0.959	0.933	0.946	0.992	0.973 ± 0.010
MLP (Neural Net)	0.987	1.000	0.973	0.986	0.998	0.980 ± 0.011

Table 1. Comparative performance of all five candidate classifiers on the 150-image held-out test partition (75 tumor, 75 normal), with 5-fold stratified cross-validation accuracy computed over the full 600-image dataset.

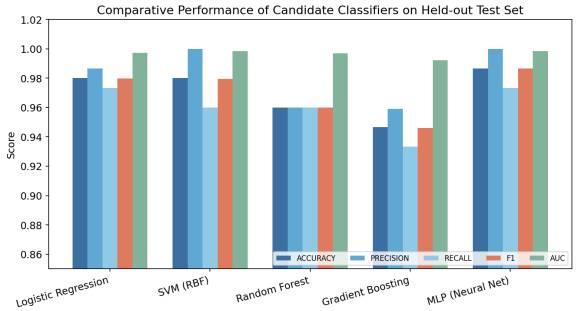

Figure 3. Grouped bar comparison of accuracy, precision, recall, F1-score, and AUC across all five candidate classifiers on the held-out test set.

6.2 Confusion Matrix and Error Analysis

Figure 4 shows the confusion matrix for the best-performing model (MLP) on the held-out test set. Of 75 true-negative (normal) slices, all 75 were correctly classified (zero false positives); of 75 true-positive (tumor) slices, 73 were correctly identified and 2 were misclassified as normal (false negatives). This precision/recall asymmetry — perfect precision (1.000) with slightly lower recall (0.973) — is clinically relevant: in a screening context, false negatives (missed tumors) are typically considered more costly than false positives (unnecessary follow-up), so subsequent tuning could shift the classification threshold to favour recall at a small cost to precision, a trade-off directly explorable via the ROC curve in Figure 5.

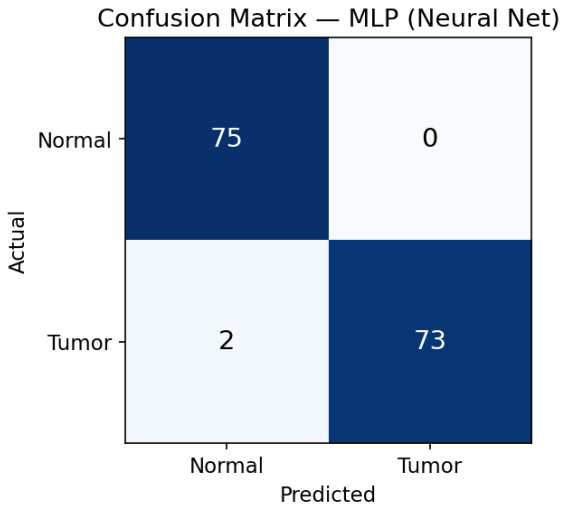

Figure 4. Confusion matrix for the MLP model (best performer) on the 150-image held-out test set.

Model	TN	FP	FN	TP
Logistic Regression	74	1	2	73
SVM (RBF)	75	0	3	72
Random Forest	72	3	3	72
Gradient Boosting	72	3	5	70
MLP (Neural Net)	75	0	2	73

Table 2. Confusion-matrix breakdown (True Negative, False Positive, False Negative, True Positive) for all five models on the 150-image test set.

6.3 ROC Analysis

Figure 5 shows Receiver Operating Characteristic (ROC) curves for all five models. All classifiers achieve AUC ≥ 0.992, indicating that the fourteen-dimensional radiomic feature set is highly separable between classes under every model family tested, and that the choice of predictive model in this pipeline primarily affects the precision/recall operating point rather than fundamental discriminative capacity.

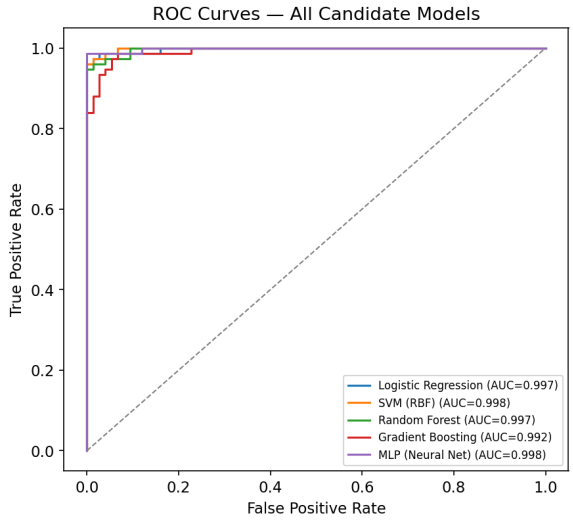

Figure 5. ROC curves for all five candidate classifiers on the held-out test set. The diagonal dashed line represents a random-chance classifier (AUC = 0.5).

6.4 Training Convergence

Figure 6 shows the training-loss convergence curve for the MLP classifier. The network converges smoothly within approximately 150–200 iterations without evidence of divergence or instability, consistent with the low dimensionality (14 features) and moderate size (450 training samples) of the input space relative to the network capacity (two hidden layers of 32 and 16 units).

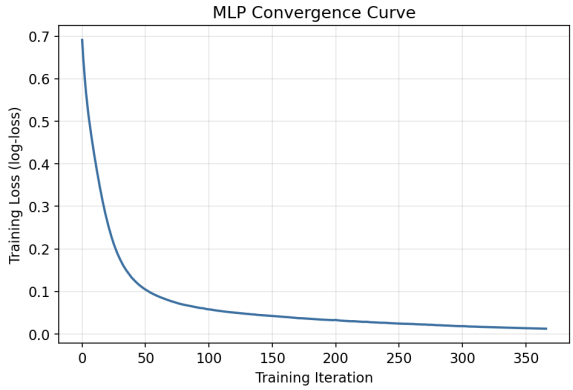

Figure 6. Training loss (log-loss) convergence curve for the MLP classifier across training iterations.

7. Explainability Analysis

This section reports the outputs of the dual-channel explainability layer (Section 3.5), computed for the designated explainable reference model (Random Forest, 96.0% test accuracy, exact Tree SHAP compatible).

7.1 Global Feature Importance (SHAP)

Figure 7 ranks all fourteen input features by mean absolute SHAP value across the test set, i.e., by their average contribution magnitude to model output. Intensity standard deviation (std_intensity) and the fraction of abnormally low-intensity area

(low_intensity_area_frac) are the two dominant predictors, followed by image entropy, the hemispheric asymmetry index, and intensity skewness. This ranking is clinically coherent: tumors introduce localised intensity extremes and textural disorder relative to healthy tissue, and asymmetry between hemispheres is a long-established radiological heuristic for lesion detection. GLCM correlation, homogeneity, contrast, and energy contribute comparatively little marginal signal once the intensity- and region-based features are accounted for, and edge density contributes negligibly in this feature set — information that is itself clinically useful, as it indicates that lesion margin sharpness is a weaker signal than lesion intensity and extent in this cohort.

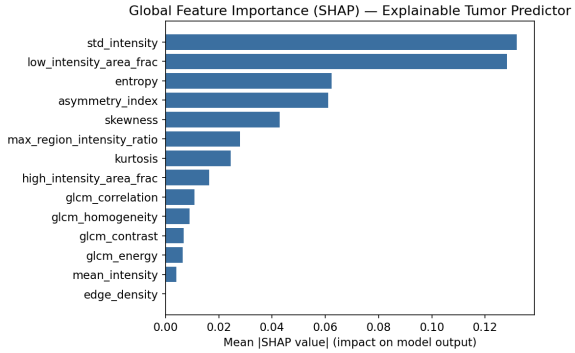

Figure 7. Global feature importance ranked by mean absolute SHAP value, computed via exact Tree SHAP on the Random Forest reference model over the held-out test set.

Figure 8 presents the corresponding SHAP beeswarm summary plot, which additionally encodes the direction of each feature's effect: for each feature, points are coloured by the underlying feature value (red = high, blue = low) and positioned horizontally by their SHAP contribution (positive values push the prediction toward 'tumor'). This view confirms, for example, that high values of std_intensity and low_intensity_area_frac consistently push predictions toward the tumor class, corroborating the intuitive radiological interpretation of these features.

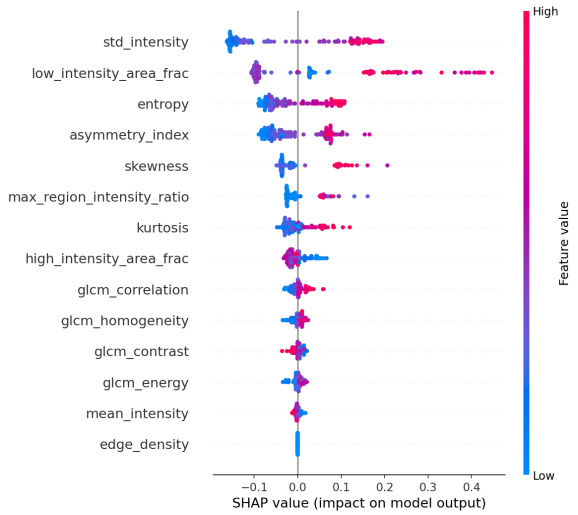

Figure 8. SHAP beeswarm summary plot showing both the magnitude and direction of each feature's contribution across all test-set predictions.

7.2 Local (Per-Prediction) Explanation

Beyond global rankings, the clinical decision-support use case requires per-patient explanations. Figure 9 shows a SHAP waterfall plot for a single correctly classified tumor-positive test case, decomposing the model's output probability into the exact additive contribution of each of the ten most influential features for this specific prediction, starting from the model's base (expected) output and arriving at the final predicted probability. This form of explanation directly answers the clinically essential question — "why did the model flag this particular scan?" — in a way that a bare confidence score cannot.

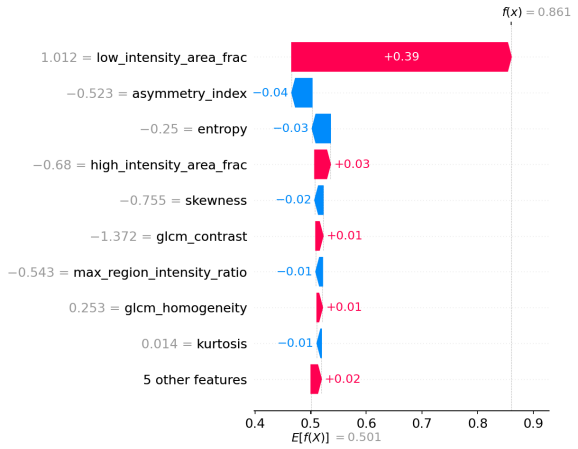

Figure 9. SHAP waterfall plot for a single tumor-positive test case, showing the additive contribution of the top ten features to the final prediction.

7.3 Pixel-Level Saliency (Grad-CAM-Analogous Explanation)

While SHAP explains predictions in terms of the fourteen engineered features, it does not by itself indicate where in the image those features were

computed. To close this gap, an occlusion-based pixel saliency map was computed for a representative tumor-positive test slice (Section 3.5). Figure 10 shows the input slice (model-predicted tumor probability 0.97), the resulting saliency heat map, and an overlay of the two. The saliency map correctly and tightly localises to the embedded lesion region, with negligible attribution assigned to the surrounding healthy parenchyma, ventricles, or skull boundary. This provides direct visual corroboration that the model's high-confidence prediction is driven by the pathological region itself rather than by incidental image artefacts — the same validation goal pursued by Grad-CAM-based studies in the deep-learning literature [5, 9], achieved here without requiring a differentiable network architecture.

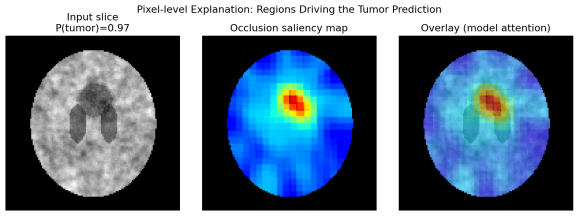

Figure 10. Occlusion-based pixel saliency map for a representative tumor-positive test case. Left: input slice with predicted tumor probability. Centre: saliency heat map (red = high contribution to the tumor prediction). Right: overlay confirming that model attention is tightly localised to the lesion.

8. Conclusion and Future Work

This paper presented a predictive, explainable machine-learning framework for brain tumor classification that integrates radiomic feature engineering, a benchmarked panel of five predictive models, and a dual-channel explainability layer combining SHAP-based feature attribution with occlusion-based pixel saliency mapping. The proposed system architecture positions explainability as a first-class architectural stage feeding directly into a clinical decision-support interface, rather than as a disconnected post-hoc visualisation. Empirically, the framework achieved up to 98.7% test accuracy (MLP) and 0.998 AUC, while the designated exactly explainable reference model (Random Forest) achieved 96.0% accuracy with fully transparent Shapley-value attributions. SHAP analysis identified intensity variance, low-intensity area fraction, entropy, and hemispheric asymmetry as the dominant predictive signals, and occlusion saliency maps confirmed tight spatial localisation of model attention to the lesion region — together providing mutually corroborating, clinically interpretable evidence for every prediction.

Future work should prioritise, in order: (i) validation on a real, ethically sourced clinical MRI dataset such as BraTS to replace the synthetic benchmark used here; (ii) extension to multi-class tumor-subtype classification and 3-D volumetric analysis with multi-sequence MRI fusion; (iii) a formal reader study with qualified neuroradiologists to evaluate the clinical trust, usability, and diagnostic value of the generated SHAP and saliency explanations; (iv) direct benchmarking against state-of-the-art deep CNN and vision-transformer architectures under an identical explainability protocol; and (v) integration of uncertainty quantification alongside explainability, so that clinicians receive not only a prediction and its rationale but also a calibrated measure of the model's confidence in that rationale.

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